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OM protein - protein search, using sw model

Run on: December 10, 2003, 20:25:06 ; Search time 11 seconds  
(without alignments)  
115.429 Million cell updates/sec

Title: US-09-936-885-3  
Perfect score: 128  
Sequence: 1 DVLKKGITVALHAGKALGAVADTISQ 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	100.0	78	1 DMS1_PHYBI	P80282 phylomedusa
2	110	85.9	34	1 DMS1_PHYSA	P24302 phylomedusa
3	105	82.0	34	1 DMS2_PHYSA	P80278 phylomedusa
4	60.5	47.3	77	1 DRG2_PHYBI	Q902k5 phylomedusa
5	55.5	43.4	76	1 DMS4_PHYBI	P81486 phylomedusa
6	53.5	41.8	81	1 DMS2_PHYBI	P31107 phylomedusa
7	52.5	41.0	81	1 DRG1_PHYBI	Q902k3 phylomedusa
8	51.5	40.2	75	1 DMS2_PACDA	Q93452 pachymedusa
9	51.5	40.2	506	1 ATP0_BETU	Q05735 beta vulgar
10	51.5	40.2	507	1 ATP0_PEA	P05493 plasma sativ
11	51.5	40.2	508	1 ATP0_MAIZE	P05494 zea mays (m
12	51.5	40.2	508	1 ATP0_PHAVU	P24459 phaseolus v
13	51.5	40.2	508	1 ATP0_SOYBN	Q01915 glycine max
14	51.5	40.2	509	1 ATP0_ORYZA	P15998 oryza sativ
15	51.5	40.2	509	1 ATP0_WHEAT	P12862 triticum ae
16	51.5	40.2	510	1 ATP0_HELAN	P18260 helianthus ae
17	51	39.8	334	1 RUVB_THEMA	Q56313 thermotoga
18	50.5	39.5	507	1 ATP0_ARATH	P92549 arabidopsis
19	50.5	39.5	507	1 ATP0_BRANA	P22201 brassica na
20	50.5	39.5	507	1 ATP0_RAPSA	P23413 raphanus sa
21	50	39.1	71	1 CER1_CERCA	P36190 ceratitidis c
22	50	39.1	71	1 CER2_CERCA	O17512 ceratitidis c
23	50	39.1	75	1 DMS3_AGRAN	Q93223 agalychnis
24	50	39.1	144	1 MAX4_BOMMX	P83083 bombyx max
25	50	39.1	417	1 YEIM_HABIN	P47472 haemophilus
26	49.5	38.7	509	1 ATP0_NICPL	P05495 nicotiana p
27	48.5	37.9	80	1 DMS3_PHYSA	P80279 phylomedusa
28	48.5	37.9	30	1 DMS3_PACDA	Q93453 pachymedusa
29	48.5	37.9	511	1 ATP0_OENBI	P05492 oenothera b
30	48	37.5	495	1 MURE_XILFA	Q95f85 xyella fas
31	47	36.7	403	1 CRE4_PSEPU	P38488 pseudomonas
32	47	36.7	697	1 SYGB_RALSO	Q8Y213 ralstonia s
33	46	35.9	71	1 CERD_CERCA	O17513 ceratitidis c

## ALIGNMENTS

## RESULT 1

ID	DMS1_PHYBI	STANDARD;	PRT;	78 AA.
AC	P80282;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Dermaseptin BI precursor (Dermaseptin BI).			
OS	Phylomedusa bicolor (Two-colored leaf frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;			
OC	Phyllomedusinae; Phyllomedusa.			
OX	NCBI_TaxID=8393;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
EX	MEDLINE=94299491; PubMed=8074751;			
RA	Amiche M., Ducancel F., Mor A., Boulain J.C., Menez A., Nicolas P.;			
RT	"Precursors of vertebrate peptide antibiotics dermaseptin b and			
RT	adenoregulin have extensive sequence identities with precursors of			
RT	opioid peptides dermorphin, dermenkephalin, and deltorphins.";			
RL	J. Biol. Chem. 269:17847-17853(1994).			
RN	(2)			
RP	SEQUENCE OF 45-75.			
RC	TISSUE=Skin secretion;			
EX	MEDLINE=94139686; PubMed=8306981;			
RA	Mor A., Nicolas P.;			
RT	"Isolation and structure of novel defensive peptides from frog skin.";			
RL	Eur. J. Biochem. 229:145-154(1994).			
CC	-1- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST			
CC	BACTERIA FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE			
CC	FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: Skin.			
CC	-1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.			
CC	Dermaseptin subfamily.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X72387; CAA51080.1; -			
DR	PIR; A53727; A53727.			
DR	PIR; B54897; B54897.			
DR	InterPro; IPR004275; Brevenin.			
DR	Pfam; PF03032; Brevenin, 1.			
KW	Amphibian defense peptide; Antibiotic; Fungicide; Multigene family;			
FT	Signal; Cleavage on pair of basic residues; Amidation.			
FT	SIGNAL 1 22 POTENTIAL.			
FT	PROPEP 23 42			
FT	CHAIN 45 75			
FT	PROPEP 76 78			
FT	DERMASEPTIN BI.			

P08155 drosophila  
P26854 marchantia  
Q17313 ceratitidis c  
P6910 mycobacteri  
Q43714 goseypitium a  
Q8xd64 escherichia  
Q46814 escherichia  
P93736 arabidopsis  
O93224 agalychnis  
P81485 phyllomedus  
Q9rn9 streptomyce  
P36191 ceratitidis c

[illegible]

Best Local Similarity 53.8%; Pred. No. 0.092; Matches 14; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 3 LKKGITVAL-HAGKAALGAVADTISQ 27

Db 51 IKEAGKAALTAAGKAALGAVSDAVE 76

# RESULT 5

DMS4\_DMSYBI STANDARD; PRT; 76 AA.

AC P81486;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Dermaseptin BIV precursor (Dermaseptin B4)

OS Phyllomedusa bicolor (Two-colored leaf frog)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;

OC Phyllomedusinae; Phyllomedusa.

NCBI\_TaxID=8393;

SEQUENCE FROM N.A., SEQUENCE OF 46-73, AND MASS SPECTROMETRY.

RP TISSUE=Skin secretion;

RC MEDLINE=98278974; PubMed=9614066;

RA Charpentier S., Amiche M., Mester J., Vouille V., Le Caer J.-P.,

RT Nicolas P., Delfour A.;

RT "Structure, synthesis, and molecular cloning of dermaseptins B, a

RT family of skin peptide antibiotics";

RL J. Biol. Chem. 273:14690-14697(1998).

CC -!- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST GRAM-

CC POSITIVE AND GRAM-NEGATIVE BACTERIA. PROBABLY ACTS BY DISTURBING

CC MEMBRANE FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.

CC -!- SUBCELLULAR LOCATION: Skin.

CC -!- TISSUE SPECIFICITY: Skin.

CC -!- MASS SPECTROMETRY: MW=2997.15; MW ERR=0.1; METHOD=Electrospray.

CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.

CC Dermaseptin subfamily.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

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DR EMBL; Y16565; CAA76289.1; -

DR InterPro; IPR004275; Brevenin.

DR Pfam; PF03032; Brevenin, 1.

KW Amphibian defense peptide; Antibiotic; Multigene family; Signal;

KW Cleavage on pair of basic residues; Amidation.

FT SIGNAL 1 22 POTENTIAL.

FT PROPEP 23 43

FT CHAIN 46 73

FT PROPEP 75 76

FT MOD RES 73 73

FT AMIDATION (G-74 PROVIDE AMIDE GROUP).

SQ SEQUENCE 76 AA; 8642 MW; A8A0525P0709F447 CRC64;

Query Match 43.4%; Score 55.5; DB 1; Length 76;

Best Local Similarity 44.4%; Pred. No. 0.45;

Matches 12; Conservative 4; Mismatches 8; Indels 3; Gaps 1;

QY 1 DVLKKGITVALHAGKAALGAVADTISQ 27

Db 50 DLKKNVGRK---AGRAVLNTVTDWVQ 73

# RESULT 6

DMS2\_DMSYBI STANDARD; PRT; 81 AA.

AC P31107; P80283;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Adenoregulin precursor (Dermaseptin B1) (Dermaseptin B2).

OS Phyllomedusa bicolor (Two-colored leaf frog)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;

OC Phyllomedusinae; Phyllomedusa.

NCBI\_TaxID=8393;

SEQUENCE FROM N.A.

RP TISSUE=Skin;

RC MEDLINE=93221546; PubMed=8466537;

RA Amiche M., Ducancel F., Lajeunesse E., Boulain J.-C., Menez A.,

RT Nicolas P.;

RT "Molecular cloning of a cDNA encoding the precursor of adenoregulin

RT from frog skin. Relationships with the vertebrate defensive peptides,

RT dermaseptins";

RL Biochem. Biophys. Res. Commun. 191:983-990(1993).

SEQUENCE OF 46-78.

RP TISSUE=Skin secretion;

RC MEDLINE=93066363; PubMed=1438301;

RA Daly J.W., Cacres J., Moni R.W., Gusovsky F., Moos M. Jr.,

RT Seamon K.B., Milton K., Myers C.W.;

RT "Frog secretions and hunting magic in the upper Amazon:

RT identification of a peptide that interacts with an adenosine

RT receptor";

RL Proc. Natl. Acad. Sci. U.S.A. 89:10960-10963(1992).

RP SYNTHESIS, AND CHARACTERIZATION.

RC TISSUE=Skin;

RX MEDLINE=94139686; PubMed=8306981;

RA Mor A., Nicolas P.;

RT "Isolation and structure of novel defensive peptides from frog skin.";

RL Eur. J. Biochem. 219:145-154(1994).

CC -!- FUNCTION: ENHANCES BINDING OF AGONISTS TO A1 ADENOSINE RECEPTORS.

CC -!- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST

CC BACTERIA, FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE

CC FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.

CC -!- DISEASE: AFFECTS HUMAN BEHAVIOR ELICITING PROFOUND MALAISE,

CC FOLLOWED BY LISTLESSNESS AND THEN EUPHORIA.

CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.

CC Dermaseptin subfamily.

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-----

DR EMBL; X70278; CAA49763.1; -

DR InterPro; IPR004275; Brevenin.

DR Pfam; PF03032; Brevenin, 1.

KW Amphibian defense peptide; Antibiotic; Fungicide; Multigene family;

KW Signal; Cleavage on pair of basic residues.

FT SIGNAL 1 22 POTENTIAL.

FT PROPEP 23 43

FT CHAIN 46 78

FT PROPEP 79 81

FT ADENOREGULIN.

SQ SEQUENCE 81 AA; 8844 MW; C26ADB4E9418272D CRC64;

Query Match 41.8%; Score 53.5; DB 1; Length 81;

Best Local Similarity 40.0%; Pred. No. 0.9;

Matches 12; Conservative 7; Mismatches 6; Indels 5; Gaps 1;

QY 3 LKKGITVALHAGKAALGAVADTISQ 27

Db 51 IKEVGKEAKAAKAAKGAALGAVSEAVE 80



RESULT 11		
ATP0	MAIZE	ATP0
ID	ATP0 MAIZE	STANDARD; PRT; 508 AA.
AC	P05494;	
DC	01-NOV-1988 (Rel. 09, Created)	
DT	01-NOV-1988 (Rel. 09, Last sequence update)	
DT	28-FEB-2003 (Rel. 41, Last annotation update)	
DE	ATP synthase alpha chain, mitochondrial (EC 3.6.3.14).	
DE	ATPA.	
GN	GN	
OS	Zea mays (Maize).	
OC	Zea mays (Maize).	
OC	Mitochondrion.	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
OC	PACCAD clade; Panicoideae; Andropogoneae; Zea.	
OX	NCBI TaxID=4577;	
OX	[1]_	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RP	Braun C.J., Levings C.S. III;	
RP	"Nucleotide sequence of the F1-ATPase alpha subunit from maize	
RT	"mitochondria.";	
RT	Plant Physiol. 79:571-577(1985).	
RL	[2]	
RL	[2]	
RP	SEQUENCE FROM N.A.	
RP	MEMLINE=88311189; PubMed=2900697;	
RR	Isaac P.G., Brennicke A., Dunbar S.M., Leaver C.J.;	
RR		







```

RL Nucleic Acids Res. 17:7531-7531 (1989).
CC -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE ALPHA CHAIN IS A REGULATORY
CC SUBUNIT.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
CC -----
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CC -----
CC EMBL; X15918; CAA34060.1; -.
CC PIR; S06007; PWTAM.
CC DR HSSP; P19483; LBMF.
CC DR InterPro; IPR000793; ATPase_a/bc.
CC DR InterPro; IPR000194; ATPase_a/bcentre.
CC DR InterPro; IPR004100; ATPase_a/bn.
CC DR InterPro; IPR000790; ATPase_ac.
CC DR InterPro; IPR005294; ATPsynthf1_alpha.
CC DR Pfam; PF00006; ATP-synt_ab; 1.
CC DR Pfam; PF00306; ATP-synt_ab_C; 1.
CC DR Pfam; PF02874; ATP-synt_ab_N; 1.
CC DR ProDom; PD001099; ATPase_ac; 1.
CC DR TIGRFAMs; TIGR00962; atpA; 1.
CC DR PROSITE; PS00152; ATPASE ALPHA BETA; 1.
CC KW ATP synthase; CF(1); Hydrogen ion transport;
CC Hydrolase; ATP-binding; Mitochondrion
CC NP_BIND 171 178 ATP (BY SIMILARITY).
CC FT ACT_SITE 373 373 BY SIMILARITY.
CC SQ SEQUENCE 509 AA; 55264 MW; 2BD7893B255EF66B CRC64;

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Query Match 40.2%; Score 51.5; DB 1; Length 509;
Best Local Similarity 42.3%; Pred. No. 8.4;
Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

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QY 1 DVLKKGITVA-LHAGKALGAVADTI 25
DB 88 DLVKTGTSIVDPVPGKALGRVVDAL 113

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Search completed: December 10, 2003, 20:28:06  
Job time : 12 secs

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OM protein - protein search, using sw model

Run on: December 10, 2003, 20:26:11 ; Search time 21 Seconds  
(without alignments)  
123.645 Million cell updates/sec

Title: US-09-936-885-3

Perfect score: 128

Sequence: 1 DVLKKTGTVALHAGKAALGAVADTISQ 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 76:\*

1: piri:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	100.0	27	2 A53727	dermaseptin b - tw
2	128	100.0	78	2 B54897	dermaseptin b i pr
3	110	85.9	34	2 A40298	dermaseptin - Sauv
4	53.5	41.8	81	1 JN0462	adenoregulin precu
5	51.5	40.2	327	4 S29876	probable H <sub>2</sub> -transp
6	51.5	40.2	506	2 S33922	H <sub>2</sub> -transporting tw
7	51.5	40.2	506	2 S46508	H <sub>2</sub> -transporting tw
8	51.5	40.2	507	2 JN0769	H <sub>2</sub> -transporting tw
9	51.5	40.2	507	2 A26760	H <sub>2</sub> -transporting tw
10	51.5	40.2	508	1 PWNAM	H <sub>2</sub> -transporting tw
11	51.5	40.2	508	2 S26979	H <sub>2</sub> -transporting tw
12	51.5	40.2	508	2 S29792	H <sub>2</sub> -transporting tw
13	51.5	40.2	509	1 PWTAM	H <sub>2</sub> -transporting tw
14	51.5	40.2	509	1 PWRZAM	H <sub>2</sub> -transporting tw
15	51.5	40.2	509	1 S1997	H <sub>2</sub> -transporting tw
16	51.5	40.2	510	2 S19261	H <sub>2</sub> -transporting tw
17	51	39.8	334	2 A72217	Holliday junction
18	50.5	39.5	507	1 PWRPA	H <sub>2</sub> -transporting tw
19	50.5	39.5	507	2 S12309	H <sub>2</sub> -transporting tw
20	50.5	39.5	590	2 A96691	arginyl-tRNA synth
21	50	38.1	417	2 A6154	hypothetical prote
22	49.5	38.7	509	1 PWNAC	H <sub>2</sub> -transporting tw
23	49	38.3	236	2 G90007	purine nucleoside
24	49	38.3	256	2 F78103	probable transcrip
25	48.5	37.9	317	2 H70805	H <sub>2</sub> -transporting tw
26	48.5	37.9	491	2 S17916	hypothetical prote
27	48.5	37.9	511	2 S7316	H <sub>2</sub> -transporting tw
28	48	37.5	396	2 H97500	hypothetical prote
29	48	37.5	396	2 AD2719	conserved hypothet.

30 48 37.5 495 2 H82762 UDP-N-acetylmurano  
31 48 37.5 694 2 E97630 hypothetical prote  
32 48 37.5 694 2 AH2853 conserved hypothet  
33 48 37.5 705 2 T18547 flax rust resistan  
34 48 37.5 718 2 A81122 hypothetical prote  
35 48 37.5 1294 2 T18546 flax rust resistan  
36 47.5 37.1 642 2 T06014 arginine-tRNA liga  
37 47 36.7 29 2 A61613 ceratotoxin A - Me  
38 47 36.7 753 2 D81219 NADH dehydrogenase  
39 47 36.7 753 2 F81991 NADH2 dehydrogenas  
40 46.5 36.3 509 2 T11937 H<sub>2</sub>-transporting tw  
41 46.5 36.3 557 2 C84146 ABC transporter re  
42 46 35.9 517 2 G75593 utrophyrin-III C  
43 45.5 35.5 513 2 S25955 H<sub>2</sub>-transporting tw  
44 45.5 35.5 558 2 E97203 2-oxoacid:ferredox  
45 45.5 35.5 1259 2 S25954 gene atpA, intron 2

#### ALIGNMENTS

##### RESULT 1

A53727

dermaseptin b - two-colored leaf frog

C/Species: Phyllomedusa bicolor (two-colored leaf frog)

C/Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 09-Apr-1998

C/Accession: A53727

R/Mor, A.; Amiche, M.; Nicolas, P.

Biochemistry 33, 6642-6650, 1994

A/Title: Structure, synthesis, and activity of dermaseptin b, a novel vertebrate defens

A/Reference number: A53727; MUID:94263975; PMID:8204601

A/Accession: A53727

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-27 <MOR>

C/Superfamily: dermaseptin precursor; dermorphin precursor amino-terminal homology

C/Keywords: skin

Query Match 100.0%; Score 128; DB 2; Length 27;

Best Local Similarity 100.0%; Pred. No. 6.9e-12;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVLKKTGTVALHAGKAALGAVADTISQ 27

DB 1 DVLKKTGTVALHAGKAALGAVADTISQ 27

##### RESULT 2

B54897

dermaseptin b I precursor - two-colored leaf frog

C/Species: Phyllomedusa bicolor (two-colored leaf frog)

C/Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 16-Jul-1999

C/Accession: B54897

R/Amiche, M.; Ducancel, F.; Mor, A.; Boulain, J.C.; Menez, A.; Nicolas, P.

J. Biol. Chem. 269, 17847-17852, 1994

A/Title: Precursors of vertebrate peptide antibiotics dermaseptin b and adenoregulin ha

A/Reference number: A54897; MUID:94299491; PMID:8074751

A/Accession: B54897

A/Molecule type: mRNA

A/Residues: 1-78 <AMI>

A/Cross-references: GB:X72387; NID:9505483; PIDN:CAAS1080.1; PID:9505484

C/Superfamily: dermaseptin precursor; dermorphin precursor amino-terminal homology

C/Keywords: amidated carboxyl end; antibiotic; antifungal; skin

F1-44/Domain: dermorphin precursor amino-terminal homology <DER>

F1-22/Domain: signal sequence #status predicted <SIG>

F23-44/Domain: propeptide #status predicted <PRO>

F49-75/Product: dermaseptin b I #status experimental <WAT>

F75/Modified site: amidated carboxyl end (Gln) (amide in mature form from following gl)

Query Match

Best Local Similarity 100.0%; Score 128; DB 2; Length 78;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Y.; Collin, S.; Davies, D.R.; Thomas, C.M.  
Mol. Biol. 25, 91-103, 1994  
A/Title: Differential screening of mitochondrial cDNA libraries from male-fertile and cy  
A/Reference number: S46505; MUID:94272017; PMID:8003700  
A/Accession: S46508  
A/Molecule type: DNA  
A/Residues: 1-506 <XUE>  
A/Cross-references: EMBL:X68691  
A/Experimental source: male-sterile CMS  
A/Note: The authors translated the codon GAT for residue 207 as Val  
A/Accession: S46507  
A/Molecule type: DNA  
A/Residues: 1-506 <XUE>  
A/Cross-references: EMBL:X68690  
A/Experimental source: male-fertile MF  
A/Note: The authors translated the codon GAT for residue 207 as Val  
R.Xue, Y.  
submitted to the EMBL Data Library, October 1992  
A/Reference number: S51586  
A/Accession: S51586  
A/Molecule type: DNA  
A/Residues: 1-447, 'L', 449, 'G', 451-453, 'D', 455-506 <XUE>  
A/Cross-references: EMBL:X68691; NID:G396759; PIDN:CAA48650.1; PID:G396760  
A/Experimental source: male-sterile CMS  
R.Xue, Y.; Davies, D.R.; Collin, S.; Thomas, C.M.  
submitted to the EMBL Data Library, October 1992  
A/Description: Molecular characterization of mitochondrial ATPase subunit A from cytopla  
A/Reference number: S29535  
A/Accession: S29535  
A/Molecule type: DNA  
A/Residues: 1-447, 'L', 449, 'G', 451-453, 'D', 455-506 <XUA>  
A/Cross-references: EMBL:X68690; NID:G11262; PIDN:CAA48649.1; PID:G11263  
A/Experimental source: male-fertile MF  
C/Genetics:  
A/Gene: atpA  
A/Genome: Mitochondrion  
C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase al  
C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; nuc  
F171-178/Region: nucleotide-binding motif A (P-loop)  
F205-377/Domain: H+-transporting ATP synthase alpha chain homology <ATP>  
Query Match 40.2%; Score 51.5; DB 2; Length 506;  
Best Local Similarity 42.3%; Pred. No. 14;  
Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
QY 1 DVLKKIGTVA-LHAGKALGAVADTI 25  
DB 88 DLVKRTGSIVDPAGKAMLGKRVVDAL 113  
RESULT 8  
JN0769  
H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - garden pea mitochondrion  
A/Alternate names: ATP synthase; ATPase; F1F0-ATPase alpha chain  
C/Species: mitochondrion Pisum sativum (garden pea)  
C/Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 03-Jun-2002  
C/Accession: JN0769  
R.Morikami, A.; Nakamura, K.  
Biochim. Biophys. Acta 1153, 1530-1535, 1993  
A/Title: Transcript map of oppositely oriented pea mitochondrial genes encoding the alph  
A/Reference number: JN0769; MUID:94033860; PMID:7764223  
A/Accession: JN0769  
A/Molecule type: DNA  
A/Residues: 1-507 <MOR>  
A/Cross-references: GB:D14698; NID:9286139; PIDN:BA03524.1; PID:9286140  
C/Comment: This enzyme is essential in the translocation of H+ through the inner mitoch  
C/Genetics:  
A/Genome: Mitochondrion  
C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase al  
C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; nuc  
F171-178/Region: nucleotide-binding motif A (P-loop)  
F205-377/Domain: H+-transporting ATP synthase alpha chain homology <ATP>

Query Match 40.2%; Score 51.5; DB 2; Length 507;  
Best Local Similarity 42.3%; Pred. No. 14;  
Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
QY 1 DVLKKIGTVA-LHAGKALGAVADTI 25  
DB 88 DLVKRTGSIVDPAGKAMLGKRVVDAL 113  
RESULT 9  
A26760  
H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - garden pea mitochondrion  
C/Species: mitochondrion Pisum sativum (garden pea)  
C/Date: 09-May-1988 #sequence\_revision 09-May-1988 #text\_change 03-Jun-2002  
C/Accession: A26760  
R.Morikami, A.; Nakamura, K.  
J. Biochem. 101, 967-976, 1987  
A/Title: Structure and expression of pea mitochondrial F1ATPase alpha-subunit gene and  
A/Reference number: A26760; MUID:87279992; PMID:2886497  
A/Accession: A26760  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-507 <MOR>  
C/Genetics:  
A/Genome: Mitochondrion  
C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase a  
C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; nuc  
F171-178/Region: nucleotide-binding motif A (P-loop)  
F205-377/Domain: H+-transporting ATP synthase alpha chain homology <ATP>  
Query Match 40.2%; Score 51.5; DB 2; Length 507;  
Best Local Similarity 42.3%; Pred. No. 14;  
Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
QY 1 DVLKKIGTVA-LHAGKALGAVADTI 25  
DB 88 DLVKRTGSIVDPAGKAMLGKRVVDAL 113  
RESULT 10  
PZMZAM  
H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - maize mitochondrion  
A/Alternate names: ATPase alpha chain  
C/Species: mitochondrion Zea mays (maize)  
C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 14-Dec-2001  
C/Accession: A23757  
R.Braun, C.J.; Levings III, C.S.  
Plant Physiol. 79, 571-577, 1985  
A/Title: Nucleotide sequence of the F1-ATPase alpha subunit gene from maize mitochondri  
A/Reference number: A23757  
A/Accession: A23757  
A/Molecule type: DNA  
A/Residues: 1-508 <BRA>  
A/Cross-references: EMBL:M16222; NID:G342633; PIDN:AAA70269.1; PID:G897619  
C/Genetics:  
A/Gene: atpA  
A/Genome: Mitochondrion  
C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase al  
C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; nuc  
F171-178/Region: nucleotide-binding motif A (P-loop)  
F205-377/Domain: H+-transporting ATP synthase alpha chain homology <ATP>  
F268-273/Region: nucleotide-binding motif B  
F177/Binding site: ATP (LYS) #status predicted  
F1376/Active site: Arg #status predicted  
Query Match 40.2%; Score 51.5; DB 1; Length 508;  
Best Local Similarity 42.3%; Pred. No. 14;  
Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
QY 1 DVLKKIGTVA-LHAGKALGAVADTI 25  
DB 88 DLVKRTGSIVDPAGKAMLGKRVVDAL 113

RESULT 11  
 S26979  
 H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - kidney bean mitochondrion  
 N/Alternate names: ATPase alpha chain  
 C/Species: mitochondrion Phaseolus vulgaris (kidney bean)  
 C/Date: 23-Apr-1993 #sequence\_revision 23-Apr-1993 #text\_change 03-Jun-2002  
 C/Accession: S26979  
 R/Chase, C.D.; Ortega, V.M.  
 Curr. Genet. 22, 147-153, 1992  
 A/Title: Organization of ATPa coding and 3' flanking sequences associated with cytoplasm  
 A/Reference number: S26979; MUID:93046798; PMID:14231717  
 A/Accession: S26979  
 A/Molecule type: DNA  
 A/Residues: 1-508 <CHA>  
 A/Cross-references: EMBL:M64246; NID:g169317; PIDN:AA01582.1; PID:g169318  
 A/Note: the authors translated the codon GGG for residue 257 as Cys  
 C/Genetics:  
 A/Gene: atpa  
 A/Genome: mitochondrion  
 C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase al  
 C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; nu  
 F/171-178/Region: nucleotide-binding motif A (P-loop)  
 F/205-377/Domain: H+-transporting ATP synthase alpha chain homology <ATP>  
 Query Match 40.2%; Score 51.5; DB 2; Length 508;  
 Best Local Similarity 42.3%; Pred. No. 14;  
 Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 DVLLKIGTVA-LHAGKAALGAVADTI 25  
 DB 88 DLVKTGTSIVDPAGKAMLGRRVVDAL 113  
 RESULT 12  
 S29792  
 H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - soybean mitochondrion  
 N/Alternate names: ATPase alpha chain  
 C/Species: mitochondrion Glycine max (soybean)  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 03-Jun-2002  
 C/Accession: S29792; S29873  
 R/Chanut, P.A.; Grabau, E.A.; Gesteland, R.P.  
 Curr. Genet. 23, 234-247, 1993  
 A/Title: Complex organization of the soybean mitochondrial genome: recombination repeats  
 A/Reference number: S29792; MUID:93169687; PMID:8435853  
 A/Accession: S29792  
 A/Molecule type: DNA  
 A/Residues: 1-508 <CHA>  
 A/Cross-references: EMBL:Z14031; NID:g22738; PIDN:CAA78407.1; PID:g22739  
 C/Genetics:  
 A/Gene: atpa  
 A/Genome: mitochondrion  
 C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase al  
 C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; nu  
 F/171-178/Region: nucleotide-binding motif A (P-loop)  
 F/205-377/Domain: H+-transporting ATP synthase alpha chain homology <ATP>  
 Query Match 40.2%; Score 51.5; DB 2; Length 508;  
 Best Local Similarity 42.3%; Pred. No. 14;  
 Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 DVLLKIGTVA-LHAGKAALGAVADTI 25  
 DB 88 DLVKTGTSIVDPAGKAMLGRRVVDAL 113  
 RESULT 13  
 PWTAM  
 H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - wheat mitochondrion  
 C/Species: mitochondrion Triticum aestivum (common wheat)  
 C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 14-Dec-2001  
 C/Accession: S06007  
 R/Schulte, E.; Staubach, S.; Laser, B.; Kueck, U.

Nucleic Acids Res. 17, 7531, 1989  
 A/Title: Wheat mitochondrial DNA: organization and sequences of the atpa and atp9 ge  
 A/Reference number: S06007; MUID:90016824; PMID:2529479  
 A/Accession: S06007  
 A/Status: translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-509 <SCH>  
 A/Cross-references: EMBL:X15918  
 C/Genetics:  
 A/Gene: atpa  
 A/Genome: mitochondrion  
 C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthas  
 C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;  
 F/171-178/Region: nucleotide-binding motif A (P-loop)  
 F/205-377/Domain: H+-transporting ATP synthase alpha chain homology <ATP>  
 F/268-273/Region: nucleotide-binding motif B  
 F/177/Binding site: ATP (Lys) #status predicted  
 F/376/Active site: Arg #status predicted  
 Query Match 40.2%; Score 51.5; DB 1; Length 509;  
 Best Local Similarity 42.3%; Pred. No. 14;  
 Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 DVLLKIGTVA-LHAGKAALGAVADTI 25  
 DB 88 DLVKTGTSIVDPAGKAMLGRRVVDAL 113  
 RESULT 14  
 PWRZAM  
 H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - rice mitochondrion  
 C/Species: mitochondrion Oryza sativa (rice)  
 C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 14-Dec-2001  
 C/Accession: JQ0411  
 R/Kadowaki, K.; Kazama, S.; Suzuki, T.  
 Nucleic Acids Res. 18, 1302, 1990  
 A/Title: Nucleotide sequence of the F1-ATPase alpha subunit gene from rice mitochond  
 A/Reference number: JQ0411; MUID:90206808; PMID:2138730  
 A/Accession: JQ0411  
 A/Molecule type: DNA  
 A/Residues: 1-509 <KAD>  
 A/Cross-references: EMBL:X51422; NID:g13958; PIDN:CAA35787.1; PID:g13959  
 C/Genetics:  
 A/Gene: atpa  
 A/Genome: mitochondrion  
 C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthas  
 C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;  
 F/171-178/Region: nucleotide-binding motif A (P-loop)  
 F/205-377/Domain: H+-transporting ATP synthase alpha chain homology <ATP>  
 F/268-273/Region: nucleotide-binding motif B  
 F/177/Binding site: ATP (Lys) #status predicted  
 F/376/Active site: Arg #status predicted  
 Query Match 40.2%; Score 51.5; DB 1; Length 509;  
 Best Local Similarity 42.3%; Pred. No. 14;  
 Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 DVLLKIGTVA-LHAGKAALGAVADTI 25  
 DB 88 DLVKTGTSIVDPAGKAMLGRRVVDAL 113  
 RESULT 15  
 S10997  
 H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - common sunflower mitoch  
 C/Species: mitochondrion Helianthus annuus (common sunflower)  
 C/Date: 18-Feb-1994 #sequence\_revision 03-Aug-1995 #text\_change 03-Jun-2002  
 C/Accession: S10997; S10974; S17799; S52010; S48854  
 R/Koehler, R.H.; Loesel, A.; Zetzsche, K.  
 Nucleic Acids Res. 18, 4588, 1990  
 A/Title: Nucleotide sequence of the F1-ATPase alpha subunit gene of sunflower mitoch  
 A/Reference number: S10997; MUID:90356396; PMID:2143817  
 A/Accession: S10997

molecule type: DNA  
 A/Residues: 1-510 <KOE>  
 A/Cross-references: EMBL:X53537; NID:g12577; PIDN:CAA37613.1; PID:g758362  
 A/Experimental source: line Baso  
 R/Siculella, L.; D'Amrosio, L.; de Tuglie, A.D.; Gallerani, R.  
 Nucleic Acids Res. 18, 4599, 1990  
 A/Title: Minor differences in the primary structures of atpa genes coded on the mtDNA of  
 A/Reference number: S10374; MUID:90356407; PMID:2143818  
 A/Accession: S10974  
 A/Molecule type: DNA  
 A/Residues: 1-510 <SIC>  
 A/Cross-references: EMBL:X52838; NID:g12988; PIDN:CAA37022.1; PID:g12989  
 A/Experimental source: strain HA89  
 R/Koehler, R.H.; Horn, R.; Loessel, A.; Zetsche, K.  
 Mol. Gen. Genet. 227, 369-376, 1991  
 A/Title: Cytoplasmic male sterility in sunflower is correlated with the co-transcription  
 A/Reference number: S16528; MUID:91326025; PMID:1714033  
 A/Accession: S17799  
 A/Status: translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-510 <KOA>  
 A/Cross-references: EMBL:X55963; NID:g12985; PIDN:CAA39428.1; PID:g12986  
 A/Experimental source: line CMSBaso  
 R/Spassova, M.; Monoger, P.; Leaver, C.J.; Petrov, P.; Atanasov, A.; Nijkamp, H.J.J.; H  
 plant Mol. Biol. 26, 1819-1831, 1994  
 A/Title: Characterisation and expression of the mitochondrial genome of a new type of cy  
 A/Reference number: S52010; MUID:95161706; PMID:7858220  
 A/Accession: S52010  
 A/Status: translation not shown  
 A/Molecule type: DNA  
 A/Residues: 293-510 <SPA>  
 A/Cross-references: EMBL:X82386; NID:g563544; PIDN:CAA57786.1; PID:g563545  
 C/Genetics:  
 A/Gene: atpa  
 A/Genome: mitochondrion  
 C/Superfamily: H<sup>+</sup>-transporting ATP synthase alpha chain; H<sup>+</sup>-transporting ATP synthase al  
 C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; nuc  
 P/171-178/Region: nucleotide-binding motif A (P-loop)  
 F/205-377/Domain: H<sup>+</sup>-transporting ATP synthase alpha chain homology <ATP>

Query Match 40.2%; Score 51.5; DB 2; Length 510;  
 Best Local Similarity 42.3%; Pred. No. 14;  
 Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 1 DVLKKGITVA-LHAGKAALGAVADTI 25  
 Db 88 DLVKTGSIQVDPAGKAMLGRRVVDAL 113

Search completed: December 10, 2003, 20:29:27  
 Job time : 22 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 10, 2003, 20:27:46 ; Search time 30 Seconds  
(without alignments)  
167.385 Million cell updates/sec

Title: US-09-936-885-3

Perfect score: 128

Sequence: 1 DVLKXIGTVALHAGKAALGAVADTISQ 27

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	100.0	31	14	US-10-038-045-13
2	110	85.9	33	9	US-09-917-340-21
3	110	85.9	33	11	US-09-908-139-23
4	110	85.9	33	15	US-10-197-954-45
5	110	85.9	34	14	US-10-038-045-7
6	105	82.0	34	9	US-09-917-340-22
7	105	82.0	34	14	US-10-038-045-8
8	99.5	77.7	32	9	US-09-030-619-201
9	73	57.0	19	14	US-10-038-045-16
10	59	46.1	30	11	US-09-908-139-20
11	55	43.0	18	14	US-10-038-045-11
12	54	42.2	29	11	US-09-908-139-19
13	54	42.2	29	11	US-09-908-139-21
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					Sequence 13, Appl
					Sequence 21, Appl
					Sequence 23, Appl
					Sequence 45, Appl
					Sequence 7, Appl
					Sequence 22, Appl
					Sequence 8, Appl
					Sequence 20, Appl
					Sequence 16, Appl
					Sequence 201, App
					Sequence 10, Appl
					Sequence 11, Appl
					Sequence 19, Appl
					Sequence 21, Appl
					Sequence 14, Appl
					Sequence 42836, A

16 48.5 37.9 30 9 US-09-917-340-23  
17 48.5 37.9 30 14 US-10-038-045-9  
18 48 37.5 171 10 US-09-764-864-1225  
19 48 37.5 1258 10 US-09-867-852-107  
20 48 37.5 1295 10 US-09-738-626-6480  
21 47.5 37.1 154 15 US-10-156-761-14882  
22 47.5 37.1 590 10 US-09-893-817-2  
23 47.5 37.1 642 10 US-09-893-817-24  
24 47 36.7 29 9 US-09-917-340-30  
25 47 36.7 288 10 US-09-738-626-4286  
26 46 35.9 445 10 US-09-738-626-3627  
27 46 35.9 557 15 US-10-156-761-9608  
28 46 35.9 1276 15 US-10-156-761-10509  
29 45 35.2 26 11 US-09-908-139-17  
30 45 35.2 97 9 US-09-887-586A-40  
31 45 35.2 97 9 US-09-903-012-40  
32 45 35.2 97 11 US-09-900-797-40  
33 45 35.2 4961 12 US-10-114-153-64  
34 44 34.4 29 9 US-09-917-340-31  
35 44 34.4 29 11 US-09-908-139-24  
36 44 34.4 2080 11 US-09-382-860-2  
37 43 33.6 240 15 US-10-156-761-14602  
38 43 33.6 385 10 US-09-738-626-3888  
39 42.5 33.2 378 10 US-09-731-872-406  
40 42.5 33.2 378 12 US-09-876-997-406  
41 42.5 33.2 910 15 US-10-156-761-11103  
42 42.5 33.2 911 10 US-09-853-754-4  
43 42.5 33.2 911 12 US-10-302-896-4  
44 42.5 33.2 911 15 US-10-227-353-4  
45 42.5 33.2 922 10 US-09-855-754-6

#### ALIGNMENTS

#### RESULT 1

US-10-038-045-13  
; Sequence 13, Application US/10038045  
; Publication No. US20020150964A1  
; GENERAL INFORMATION:  
; APPLICANT: Mor, Amram  
; Vouldoukis, Ioannis  
; Nicolas, Pierre  
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
; OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/038,045  
; FILING DATE: 02-Jan-2002  
; CLASSIFICATION: <Unknown>  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US/09/181,941  
; FILING DATE: 28-Oct-1998  
; APPLICATION NUMBER: US 08/574,701  
; FILING DATE: 19-DEC-1995  
; APPLICATION NUMBER: FR 95 07831  
; FILING DATE: 29-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 3909-0021-999

Sequence 23, Appl  
Sequence 9, Appl  
Sequence 1225, Ap  
Sequence 107, App  
Sequence 6480, Ap  
Sequence 14882, A  
Sequence 2, Appl  
Sequence 24, Appl  
Sequence 30, Appl  
Sequence 4286, Ap  
Sequence 3627, Ap  
Sequence 9608, Ap  
Sequence 10509, A  
Sequence 17, Appl  
Sequence 40, Appl  
Sequence 40, Appl  
Sequence 64, Appl  
Sequence 31, Appl  
Sequence 24, Appl  
Sequence 2, Appl  
Sequence 14602, A  
Sequence 3888, Ap  
Sequence 406, App  
Sequence 406, App  
Sequence 11103, A  
Sequence 4, Appl  
Sequence 4, Appl  
Sequence 4, Appl  
Sequence 6, Appl

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. US20020150964A1e  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-10-038-045-13

Query Match 100.0%; Score 128; DB 14; Length 31;  
Best Local Similarity 100.0%; Pred. No. 4.6e-13;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVLKKGITVALHAGKAALGAVADTISQ 27  
DB 5 DVLKKGITVALHAGKAALGAVADTISQ 31

## RESULT 2

US-09-917-340-21  
Sequence 21, Application US/09917340  
Patent No. US20020090369A1  
GENERAL INFORMATION:  
APPLICANT: Murphy, Christopher J.  
APPLICANT: McAnulty, Jonathan F.  
APPLICANT: Reid, Ted W.  
TITLE OF INVENTION: Transplant Media  
FILE REFERENCE: TPLANT-06468  
CURRENT APPLICATION NUMBER: US/09/917,340  
CURRENT FILING DATE: 2001-07-29  
PRIOR APPLICATION NUMBER: 60/221,632  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: 60/249,602  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/290,932  
PRIOR FILING DATE: 2001-05-15  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 21  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Phyllomedusa sauvagae  
US-09-917-340-21

Query Match 85.9%; Score 110; DB 9; Length 33;  
Best Local Similarity 84.6%; Pred. No. 3.2e-10;  
Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VLKKGITVALHAGKAALGAVADTISQ 27  
DB 6 MLKKGITVALHAGKAALGAAADTISQ 31

## RESULT 3

US-09-908-139-23  
Sequence 23, Application US/09908139  
Publication No. US2003009694A1  
GENERAL INFORMATION:  
APPLICANT: Hancock, Robert E. W.  
APPLICANT: Gough, Monisha A.  
APPLICANT: Patrzykat, Aleksander  
APPLICANT: Woods, Donald  
APPLICANT: Jia, Xiaoyan  
TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC  
PEPTIDES AND METHODS OF USE THEREFOR  
FILE REFERENCE: 07422/016001  
CURRENT APPLICATION NUMBER: US/09/908,139  
CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: 09/143,124  
PRIOR FILING DATE: 1998-08-28  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 23  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: antimicrobial cationic peptide  
US-09-908-139-23

Query Match 85.9%; Score 110; DB 11; Length 33;  
Best Local Similarity 84.6%; Pred. No. 3.2e-10;  
Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VLKKGITVALHAGKAALGAVADTISQ 27  
DB 6 MLKKGITVALHAGKAALGAAADTISQ 31

## RESULT 4

US-10-197-954-45  
Sequence 45, Application US/10197954  
Publication No. US20030119021A1  
GENERAL INFORMATION:  
APPLICANT: K'ater, Hubert  
APPLICANT: Siddiqi, Suhail  
APPLICANT: Little, Daniel  
TITLE OF INVENTION: Capture Compounds, Collections Thereof  
TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex  
TITLE OF INVENTION: Compositions  
FILE REFERENCE: 24743-2305  
CURRENT APPLICATION NUMBER: US/10/197,954  
CURRENT FILING DATE: 2002-07-16  
PRIOR APPLICATION NUMBER: 60/306,019  
PRIOR FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: 60/314,123  
PRIOR FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: 60/363,433  
PRIOR FILING DATE: 2002-03-11  
NUMBER OF SEQ ID NOS: 149  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 45  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-197-954-45

Query Match 85.9%; Score 110; DB 15; Length 33;  
Best Local Similarity 84.6%; Pred. No. 3.2e-10;  
Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VLKKGITVALHAGKAALGAVADTISQ 27  
DB 6 MLKKGITVALHAGKAALGAAADTISQ 31

## RESULT 5

US-10-038-045-7  
Sequence 7, Application US/10038045  
Publication No. US20020150964A1  
GENERAL INFORMATION:  
APPLICANT: Mor, Anram  
APPLICANT: Vouldoukis, Ioannis  
APPLICANT: Nicolas, Pierre  
TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York



```
Best Local Similarity   80.8%; Pred. No. 2e-09;
Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0
```

Qy 2 VLKIGTVALHAGKAALGAVADTISQ 27  
 :|:|:|:|:|:|:|:|:|:|:|:|:  
Db 6 MLKKLTMALHAGKAALGAANTISQ 31

RESULT 7  
US-10-Q38-045-8  
Sequence 8, Application US/10038045  
Publication No. US20020150964A1  
GENERAL INFORMATION:  
APPLICANT: Mor, Amram  
Vouldoukis, Ioannis  
Nicolas, Pierre  
TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
NUMBER OF SEQUENCES: 16.  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION NUMBER: US/10/038,045  
APPLICATION NUMBER: US/10/038,045  
FILING DATE: 02-Jan-2002  
CLASSIFICATION: <Unknown>  
PREVIOUS APPLICATION DATA:

Length 34;  
Indels 0; Gaps 0

```

; ; REFERENCE/DOCKET NUMBER: 3309-0021-999
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: 650-493-4935
; ; TELEFAX: 650-493-5556
; ; TELEX: 66141 PENNIE
; ; INFORMATION FOR SEQ ID NO: 8:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 34 amino acids
; ; TYPE: amino acid
; ; STRANDEDNESS: single
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: NO. US20020150964ale
; ; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-038-045-8

Query Match 82.0%; Score 105; DB 14; Length 34;
Best Local Similarity 80.8; Pred. No. 2e-09;
Matches 21; Conservative 4; Mismatches 1; Indels

QY 2 VLKIGTVALHAGKAALGAVADTISQ 27
      :|||:|||||:|||||:|||||
DB 6 MLKIGTVALHAGKAALGAAVTISQ 31
      :|||:|||||:|||||:|||||

RESULT 8
US-09-030-619-201

```

length 34;

```

; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfle, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H. P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030.619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 201
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Phyllomedusa sauvagii
US-09-030-619-201

Query Match 77.7%; Score 99.5; DB 9; Length 32;
Best Local Similarity 84.6%; Pred. No. 1.4e-08;
Matches 22; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 2 VLKKGITVALHAGKAALGAVADTISQ 27
DB 6 MLKKGITMALHAGKAALGA-ADTISQ 30

RESULT 9
US-10-038-045-16
; Sequence 16, Application US/10038045
; Publication No. US20020150964A1
; GENERAL INFORMATION:
; APPLICANT: Mor, Amram
; APPLICANT: Vouldoukis, Ioannis
; APPLICANT: Nicolas, Pierre
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
; OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/038.045
; FILING DATE: 02-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; APPLICATION DATE:
; FILING DATE: 28-Oct-1998
; APPLICATION NUMBER: US 08/574,701
; FILING DATE: 19-DEC-1995
; APPLICATION NUMBER: FR 95 07831
; FILING DATE: 29-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cortuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 3909-0021-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 16:

```

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-038-045-16

Query Match 57.0%; Score 73; DB 14; Length 19;
Best Local Similarity 93.8%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 HAGKAALGAVADTISQ 27
DB 1 HAGKAALGAAADTISQ 16

RESULT 10
US-09-908-139-20
; Sequence 20, Application US/09908139
; Publication No. US20030096949A1
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha A.
; APPLICANT: Patrzykat, Aleksander
; APPLICANT: Woods, Donald
; APPLICANT: Jia, Xiaoyan
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
; TITLE OF INVENTION: PEPTIDES AND METHODS OF USE THEREFOR
; FILE REFERENCE: 07422/016001
; CURRENT APPLICATION NUMBER: US/09/908.139
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/143,124
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
US-09-908-139-20

Query Match 46.1%; Score 59; DB 11; Length 30;
Best Local Similarity 61.9%; Pred. No. 0.028;
Matches 13; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 VLKKGITVALHAGKAALGAVA 22
DB 6 MLKKAHVGKHKVKAALGAA 26

RESULT 11
US-10-038-045-11
; Sequence 11, Application US/10038045
; Publication No. US20020150964A1
; GENERAL INFORMATION:
; APPLICANT: Mor, Amram
; APPLICANT: Vouldoukis, Ioannis
; APPLICANT: Nicolas, Pierre
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
; OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

```

COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/038,045  
FILING DATE: 02-Jan-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/181,941  
FILING DATE: 28-Oct-1998  
APPLICATION NUMBER: US 08/574,701  
FILING DATE: 19-DEC-1995  
APPLICATION NUMBER: FR 95 07831  
FILING DATE: 29-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 3909-0021-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. US20020150964A1e  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-10-038-045-11

Query Match 43.0%; Score 55; DB 14; Length 18;  
Best Local Similarity 76.9%; Pred. No. 0.065;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLKIGTVALHAG 14  
DB 6 MLKLGTVLHAG 18

RESULT 12  
US-09-908-139-19  
; Sequence 19, Application US/09908139  
; Publication No. US20030096949A1  
; GENERAL INFORMATION:  
; APPLICANT: Hancock, Robert E. W.  
; APPLICANT: Gough, Monisha A.  
; APPLICANT: Patrzykat, Aleksander  
; APPLICANT: Woods, Donald  
; APPLICANT: Jia, Xiaoyan  
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC  
; TITLE OF INVENTION: PEPTIDES AND METHODS OF USE THEREFOR  
; FILE REFERENCE: 07422/016001  
; CURRENT APPLICATION NUMBER: US/09/908,139  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: 09/143,124  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 29  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antimicrobial cationic peptide  
US-09-908-139-19

Query Match 42.2%; Score 54; DB 11; Length 29;  
Best Local Similarity 63.2%; Pred. No. 0.16;  
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 KKIGTVALHAGKALGAVA 22

DB 7 KKAHVGVKGVKALGAAA 25  
RESULT 13  
US-09-908-139-21  
; Sequence 21, Application US/09908139  
; Publication No. US20030096949A1  
; GENERAL INFORMATION:  
; APPLICANT: Hancock, Robert E. W.  
; APPLICANT: Gough, Monisha A.  
; APPLICANT: Patrzykat, Aleksander  
; APPLICANT: Woods, Donald  
; APPLICANT: Jia, Xiaoyan  
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC  
; TITLE OF INVENTION: PEPTIDES AND METHODS OF USE THEREFOR  
; FILE REFERENCE: 07422/016001  
; CURRENT APPLICATION NUMBER: US/09/908,139  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: 09/143,124  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 29  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antimicrobial cationic peptide  
US-09-908-139-21

Query Match 42.2%; Score 54; DB 11; Length 29;  
Best Local Similarity 63.2%; Pred. No. 0.16;  
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 KKIGTVALHAGKALGAVA 22  
DB 7 KKAHVGVKGVKALGAAA 25

RESULT 14  
US-10-038-045-14  
; Sequence 14, Application US/10038045  
; Publication No. US20020150964A1  
; GENERAL INFORMATION:  
; APPLICANT: Mor, Amram  
; APPLICANT: Voulgoukis, Ioannis  
; APPLICANT: Nicolas, Pierre  
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
; TITLE OF INVENTION: OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/038,045  
; FILING DATE: 02-Jan-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/181,941  
; FILING DATE: 28-Oct-1998  
; APPLICATION NUMBER: US 08/574,701  
; FILING DATE: 19-DEC-1995  
; APPLICATION NUMBER: FR 95 07831

;; FILING DATE: 29-JUN-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Coruzzi, Laura A  
;; REGISTRATION NUMBER: 30,742  
;; REFERENCE/DOCKET NUMBER: 3909-0021-999  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650-493-4935  
;; TELEFAX: 650-493-5556  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 14:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 33 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: No. US20020150964A1e  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-10-038-045-14

Query Match 40.2%; Score 51.5; DB 14; Length 33;  
Best Local Similarity 42.9%; Pred. No. 0.46;  
Matches 12; Conservative 6; Mismatches 5; Indels 5; Gaps 1;

QY 3 LKIG-----TVALHAGKAAAGAVADTI 25  
DB 6 IKEVGKAAVAAKAAAGKAAAGAVSEAV 33

RESULT 15  
US-09-864-761-42836  
; Sequence 42836, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aomicca-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687

;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: US 09/608,408  
;; PRIOR FILING DATE: 2000-06-30  
;; PRIOR APPLICATION NUMBER: US 09/774,203  
;; PRIOR FILING DATE: 2001-01-29  
;; NUMBER OF SEQ ID NOS: 49117  
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
;; SEQ ID NO 42836  
;; LENGTH: 287  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: MAP TO AL049870.1  
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.6  
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7  
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.2  
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96  
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.98  
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.98  
;; OTHER INFORMATION: EST HUMAN HIT: U69560.1, EVALUE 3.00e-55  
;; OTHER INFORMATION: SWISSPROT HIT: Q04652, EVALUE 3.00e-57  
US-09-864-761-42836

Query Match 38.3%; Score 49; DB 9; Length 287;  
Best Local Similarity 36.4%; Pred. No. 14;  
Matches 8; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 DVLKKIGTVLHAGKAAAGAVA 22  
DB 36 DIILRVGDVKIHAKVVLASVS 57

Search completed: December 10, 2003, 20:30:44  
Job time : 30 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 10, 2003, 20:26:51 / Search time 21 Seconds  
(without alignments)  
54.400 Million cell updates/sec

Title: US-09-936-885-3

Perfect score: 128

Sequence: 1 DVLKXIGTVALHAGKAALGAVADTISQ 27

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:

1: /cgn2.6/ptodata/1/iaa/5A COMB.pdp.\*  
2: /cgn2.6/ptodata/1/iaa/5B COMB.pdp.\*  
3: /cgn2.6/ptodata/1/iaa/6A COMB.pdp.\*  
4: /cgn2.6/ptodata/1/iaa/6B COMB.pdp.\*  
5: /cgn2.6/ptodata/1/iaa/6C COMB.pdp.\*  
6: /cgn2.6/ptodata/1/iaa/6D COMB.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	100.0	31	4	US-09-181-941-13
2	110	85.9	33	3	US-09-143-124-23
3	110	85.9	34	4	US-09-181-941-7
4	105	82.0	34	4	US-09-181-941-8
5	99.5	77.7	32	4	US-09-030-619-201
6	73	57.0	19	4	US-09-181-941-16
7	59	46.1	30	3	US-09-143-124-20
8	55	43.0	18	4	US-09-181-941-11
9	54	42.2	29	3	US-09-143-124-19
10	54	42.2	29	3	US-09-143-124-21
11	51.5	40.2	33	4	US-09-181-941-14
12	49	38.3	265	4	US-09-252-991A-24310
13	48.5	37.9	30	4	US-09-181-941-9
14	48	37.5	1209	5	PCR-US95-04589-107
15	48	37.5	1258	2	US-08-310-912A-107
16	48	37.5	1258	3	US-09-301-085-107
17	48	37.5	1294	3	US-08-930-996A-10
18	45.5	35.5	625	4	US-09-252-991A-23005
19	45	35.2	26	3	US-09-143-124-17
20	45	35.2	97	4	US-09-398-395A-40
21	45	35.2	97	4	US-09-887-586A-40
22	45	35.2	97	4	US-09-895-752-40
23	45	35.2	97	4	US-09-903-012B-40
24	45	35.2	926	4	US-09-252-991A-31053
25	44	34.4	29	3	US-09-143-124-24
26	44	34.4	1039	4	US-09-252-991A-28966
27	43.5	34.0	566	4	US-09-252-991A-24498

28	43.5	34.0	858	4	US-09-252-991A-17399	Sequence 17399, A
29	43	33.6	292	4	US-09-107-532A-5310	Sequence 5310, Ap
30	43	33.6	404	4	US-09-328-352-6747	Sequence 6747, Ap
31	43	33.6	1584	3	US-09-251-645-6	Sequence 6, Appl
32	42.5	33.2	469	4	US-09-252-991A-29009	Sequence 29009, A
33	42.5	33.2	911	3	US-08-460-269C-4	Sequence 4, Appl
34	42.5	33.2	922	3	US-08-460-269C-6	Sequence 6, Appl
35	42	32.8	27	4	US-09-030-619-170	Sequence 170, Appl
36	42	32.8	80	2	US-08-849-373-5	Sequence 5, Appl
37	42	32.8	116	4	US-09-199-637A-409	Sequence 409, Appl
38	42	32.8	359	4	US-09-252-991A-23051	Sequence 23051, A
39	42	32.8	383	4	US-09-252-991A-18049	Sequence 18049, A
40	42	32.8	400	4	US-08-311-731A-81	Sequence 81, Appl
41	42	32.8	409	4	US-08-311-731A-188	Sequence 188, Appl
42	42	32.8	458	4	US-09-252-991A-28585	Sequence 28585, A
43	42	32.8	501	4	US-09-328-352-5227	Sequence 3227, Ap
44	42	32.8	536	4	US-09-252-991A-33121	Sequence 33121, A
45	42	32.8	685	4	US-09-252-991A-31711	Sequence 31711, A

#### ALIGNMENTS

#### RESULT 1

US-09-181-941-13

/ Sequence 13, Application US/09181941

/ Patent No. 6440690

/ GENERAL INFORMATION:

/ APPLICANT: Mor, Amram

/ Vouldoukis, Ioannis

/ Nicolas, Pierre

/ TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION

/ NUMBER OF SEQUENCES: 16

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Pennie & Edmonds LLP

/ CITY: New York

/ STATE: NY

/ COUNTRY: USA

/ ZIP: 10036-2811

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Diskette

/ OPERATING SYSTEM: Windows

/ SOFTWARE: FastSeq for Windows Version 2.0b

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/181,941

/ FILING DATE: 28-Oct-1998

/ CLASSIFICATION: <Unknown>

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/574,701

/ FILING DATE: 19-DEC-1995

/ APPLICATION NUMBER: FR 95 07831

/ FILING DATE: 29-JUN-1995

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Coruzzi, Laura A

/ REGISTRATION NUMBER: 30,742

/ REFERENCE/DOCKET NUMBER: 3909-0021-999

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 650-493-4935

/ TELEFAX: 650-493-5556

/ TELEX: 66141 PENNIE

/ INFORMATION FOR SEQ ID NO: 13:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 31 amino acids

/ TYPE: amino acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: No. 6440690e

/ SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-181-941-13

Query Match 100.0%; Score 128; DB 4; Length 31;  
Best Local Similarity 100.0%; Pred. No. 6.9e-14;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVLKKIGTVALHAGKAALGAVADTISQ 27  
DB 5 DVLKKIGTVALHAGKAALGAVADTISQ 31

RESULT 2  
US-09-143-124-23  
; Sequence 23, Application US/09143124  
; Patent No. 6288212  
; GENERAL INFORMATION:  
; APPLICANT: Hancock, Robert E. W.  
; APPLICANT: Gough, Monisha A.  
; APPLICANT: Patrzykat, Aleksander  
; APPLICANT: Woods, Donald  
; APPLICANT: Jia, Xiaoyan  
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC  
; TITLE OF INVENTION: PEPTIDES AND METHODS OF USE THEREFOR  
; FILE REFERENCE: 07422/016001  
; CURRENT APPLICATION NUMBER: US/09/143,124  
; CURRENT FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antimicrobial cationic peptide  
US-09-143-124-23

Query Match 85.9%; Score 110; DB 3; Length 33;  
Best Local Similarity 84.6%; Pred. No. 5.7e-11;  
Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VLKKGITVALHAGKAALGAVADTISQ 27  
DB 6 MLKKLGTMALHAGKAALGAAADTISQ 31

RESULT 3  
US-09-181-941-7  
; Sequence 7, Application US/09181941  
; Patent No. 6440690  
; GENERAL INFORMATION:  
; APPLICANT: Mor, Amram  
; APPLICANT: Vouldoukis, Ioannis  
; APPLICANT: Nicolas, Pierre  
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
; OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/181,941  
; FILING DATE: 28-Oct-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/574,701  
; FILING DATE: 19-DEC-1995

APPLICATION NUMBER: FR 95 07831  
FILING DATE: 29-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 3909-0021-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6440690e  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-181-941-7

Query Match 85.9%; Score 110; DB 4; Length 34;  
Best Local Similarity 84.6%; Pred. No. 5.9e-11;  
Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VLKKGITVALHAGKAALGAVADTISQ 27  
DB 6 MLKKLGTMALHAGKAALGAAADTISQ 31

RESULT 4  
US-09-181-941-8  
; Sequence 8, Application US/09181941  
; Patent No. 6440690  
; GENERAL INFORMATION:  
; APPLICANT: Mor, Amram  
; APPLICANT: Vouldoukis, Ioannis  
; APPLICANT: Nicolas, Pierre  
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
; OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/181,941  
; FILING DATE: 28-Oct-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/574,701  
; FILING DATE: 19-DEC-1995  
; APPLICATION NUMBER: FR 95 07831  
; FILING DATE: 29-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 3909-0021-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6440690e  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-181-941-8

Query Match 82.0%; Score 105; DB 4; Length 34;  
Best Local Similarity 80.8%; Pred. No. 3.7e-10;  
Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 VLKKGITVALHAGKALGAAVADTISQ 27  
Db 6 MLKKGITVALHAGKALGAAVADTISQ 31

RESULT 5  
US-09-030-619-201  
; Sequence 201, Application US/09030619B  
; Patent No. 6503881  
; GENERAL INFORMATION:  
; APPLICANT: Kriesger, Timothy J.  
; APPLICANT: Taylor, Robert  
; APPLICANT: Erfile, Douglas  
; APPLICANT: Fraser, Janet R.  
; APPLICANT: West, Michael H.P.  
; APPLICANT: McNicol, Patricia J.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING  
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION  
; TITLE OF INVENTION: WITH ANTIBIOTICS  
; FILE REFERENCE: 660081.406  
; CURRENT APPLICATION NUMBER: US/09/030,619B  
; CURRENT FILING DATE: 1998-02-25  
; NUMBER OF SEQ ID NOS: 232  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 201  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Phyllomedusa sauvaigi  
US-09-030-619-201

Query Match 77.7%; Score 99.5; DB 4; Length 32;  
Best Local Similarity 84.6%; Pred. No. 2.6e-09;  
Matches 22; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 2 VLKKGITVALHAGKALGAAVADTISQ 27  
Db 6 MLKKGITVALHAGKALGAAVADTISQ 30

RESULT 6  
US-09-181-941-16  
; Sequence 16, Application US/09181941  
; Patent No. 6440690  
; GENERAL INFORMATION:  
; APPLICANT: Mor, Amram  
; APPLICANT: Vouloudakis, Ioannis  
; APPLICANT: Nicolas, Pierre  
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
; TITLE OF INVENTION: OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/181,941  
FILING DATE: 28-Oct-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/574,701  
FILING DATE: 19-DEC-1995  
APPLICATION NUMBER: FR 95 07831  
FILING DATE: 29-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 3909-0021-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-181-941-16

Query Match 57.0%; Score 73; DB 4; Length 19;  
Best Local Similarity 93.8%; Pred. No. 2.5e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 HAGKALGAAVADTISQ 27  
Db 1 HAGKALGAAVADTISQ 16

RESULT 7  
US-09-143-124-20  
; Sequence 20, Application US/09143124  
; Patent No. 6288212  
; GENERAL INFORMATION:  
; APPLICANT: Hancock, Robert E. W.  
; APPLICANT: Gough, Monisha A.  
; APPLICANT: Patrzykat, Aleksander  
; APPLICANT: Woods, Donald  
; APPLICANT: Jia, Xiaoyan  
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC  
; TITLE OF INVENTION: PEPTIDES AND METHODS OF USE THEREFOR  
; FILE REFERENCE: 07422/016001  
; CURRENT APPLICATION NUMBER: US/09/143,124  
; CURRENT FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antimicrobial cationic peptide  
US-09-143-124-20

Query Match 46.1%; Score 59; DB 3; Length 30;  
Best Local Similarity 61.9%; Pred. No. 0.0074;  
Matches 13; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 VLKKGITVALHAGKALGAAV 22  
Db 6 MLKKAARVGHVGAALGAAA 26

RESULT 8  
US-09-181-941-11  
; Sequence 11, Application US/09181941  
; Patent No. 6440690  
; GENERAL INFORMATION:

```
; APPLICANT: Mor, Amram
; Vouldoukis, Ioannis
; Nicolas, Pierre
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
; OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/181,941
; FILING DATE: 28-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/574,701
; FILING DATE: 19-DEC-1995
; APPLICATION NUMBER: PR 95 07831
; FILING DATE: 29-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 3909-0021-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5536
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-181-941-11
;
; QUERY MATCH 43.0%; Score 55; DB 4; Length 18;
; Best Local Similarity 76.9%; Pred. No. 0.018;
; Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
;
QY 2 VLKKIGTVALHAG 14
;
Db 6 MLKKIGTVALHAG 18
;
; RESULT 9
; US-09-143-124-19
; Sequence 19, Application US/09143124
; Patent No. 6288212
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha A.
; APPLICANT: Patrzykat, Aleksander
; APPLICANT: Woods, Donald
; APPLICANT: Jia, Xiaoyan
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
; FILE REFERENCE: 07422/016001
; CURRENT APPLICATION NUMBER: US/09/143,124
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 29
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6440690e
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-181-941-11
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
US-09-143-124-19
;
; QUERY MATCH 42.2%; Score 54; DB 3; Length 29;
; Best Local Similarity 63.2%; Pred. No. 0.045;
; Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
;
QY 4 KKIGTVALHAGKAAALGAVA 22
;
Db 7 KKAHVGVKHKVGAALGAAA 25
;
; RESULT 10
; US-09-143-124-21
; Sequence 21, Application US/09143124
; Patent No. 6288212
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha A.
; APPLICANT: Patrzykat, Aleksander
; APPLICANT: Woods, Donald
; APPLICANT: Jia, Xiaoyan
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
; FILE REFERENCE: 07422/016001
; CURRENT APPLICATION NUMBER: US/09/143,124
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
US-09-143-124-21
;
; QUERY MATCH 42.2%; Score 54; DB 3; Length 29;
; Best Local Similarity 63.2%; Pred. No. 0.045;
; Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
;
QY 4 KKIGTVALHAGKAAALGAVA 22
;
Db 7 KKAHVGVKHKVGAALGAAA 25
;
; RESULT 11
; US-09-181-941-14
; Sequence 14, Application US/09181941
; Patent No. 6440690
; GENERAL INFORMATION:
; APPLICANT: Mor, Amram
; Vouldoukis, Ioannis
; Nicolas, Pierre
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
; OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/181,941
; FILING DATE: 28-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/574,701
; FILING DATE: 19-DEC-1995
; APPLICATION NUMBER: PR 95 07831
; FILING DATE: 29-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 3909-0021-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5536
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-181-941-11
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APPLICATION NUMBER: US/09/181,941  
FILING DATE: 28-Oct-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/574,701  
FILING DATE: 19-DEC-1995  
APPLICATION NUMBER: FR 95 07831  
FILING DATE: 29-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 3909-0021-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6440690e  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-181-941-14

Query Match 40.2%; Score 51.5; DB 4; Length 33;  
Best Local Similarity 42.9%; Pred. No. 0.13;  
Matches 12; Conservative 6; Mismatches 5; Indels 5; Gaps 1;

QY 3 LKIG-----TVALHAGKAAALGAVADTI 25  
DB 6 IREVGKEAAKAAKAAKAAALGAVSEAV 33

RESULT 12  
US-09-252-991A-24310  
Sequence 24310, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 24310  
LENGTH: 265  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-24310

Query Match 38.3%; Score 49; DB 4; Length 265;  
Best Local Similarity 37.5%; Pred. No. 3.8;  
Matches 12; Conservative 5; Mismatches 5; Indels 10; Gaps 1;

QY 6 IGTVLH-----AGKAAALGAVADTISQ 27  
DB 228 LGSVALHWPRDQDCVRRVRRHGLTADTVSQ 259

RESULT 13  
US-09-181-941-9  
Sequence 9, Application US/09181941  
Patent No. 6440690  
GENERAL INFORMATION:  
APPLICANT: Mor, Amram  
Vouldoukis, Ioannis

Nicolas, Pierre  
TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/181,941  
FILING DATE: 28-Oct-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/574,701  
FILING DATE: 19-DEC-1995  
APPLICATION NUMBER: FR 95 07831  
FILING DATE: 29-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 3909-0021-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6440690e  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-181-941-9

Query Match 37.9%; Score 48.5; DB 4; Length 30;  
Best Local Similarity 61.9%; Pred. No. 0.36;  
Matches 13; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 1 DVLKKTGTVALHAGKAAALGAV 21  
DB 5 NMLKGIGKL---AGKAAALGAV 22

RESULT 14  
PCT-US95-04589-107  
Sequence 107, Application PC/TUS9504589  
GENERAL INFORMATION:  
APPLICANT: Ausubel, Frederick M.  
APPLICANT: Staskawicz, Brian J.  
APPLICANT: Brent, Andrew F.  
APPLICANT: Dahlbeck, Douglas  
APPLICANT: Katagiri, Fumiaki  
APPLICANT: Kunkel, Barbara N.  
APPLICANT: Mindrinos, Michael N.  
APPLICANT: Yu, Guo-Liang  
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF  
NUMBER OF SEQUENCES: 201  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street Suite 3100  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2904

. RESULT 15  
 US-08-310-912A-107  
 / Sequence 107, Application US/08310912A  
 / Patent No. 5981730  
 / GENERAL INFORMATION:  
 / APPLICANT: Ausubel, Frederick M.  
 / APPLICANT: Staskawicz, Brian J.  
 / APPLICANT: Brent, Andrew F.  
 / APPLICANT: Dahlbeck, Douglas  
 / APPLICANT: Katagiri, Fumitaki  
 / APPLICANT: Kunkel, Barbara N.  
 / APPLICANT: Mindrinos, Michael N.  
 / APPLICANT: Yu, Guo-Liang  
 / TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION  
 /  
 / TITLE OF INVENTION: METHODS  
 / NUMBER OF SEQUENCES: 208  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESS: Fish & Richardson P.C.  
 / STREET: 225 Franklin Street  
 / CITY: Boston  
 / STATE: MA  
 / COUNTRY: USA  
 / ZIP: 02110-2904  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: PatentIn Release #1.0, Version #1.308  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/310.912A  
 / FILING DATE: September 22, 1994  
 / CLASSIFICATION: 536  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: 08/227,360  
 / FILING DATE: April 13, 1994

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 10, 2003, 20:24:16 / Search time 42 seconds  
(without alignments)  
102.039 Million cell updates/sec

Title: US-09-936-885-3

Perfect score: 128

Sequence: 1 DVLKIGTVALHAGKAALCAVADTTISQ 27

Scoring table: BLOSUM62

Gapop 10.0 , Capext -0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.\*

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- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
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- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
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- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	100.0	27	21	AA18725 Amino acid sequenc
2	128	100.0	31	21	AA18726 Amino acid sequenc
3	128	100.0	31	21	AA12436 Dermaseptin B amin
4	128	100.0	32	21	AA18748 A mature dermaspt
5	128	100.0	78	21	AA18724 A dermasptin prec
6	110	85.9	33	21	AA18730 Cationic antimicro
7	110	85.9	33	23	AAU90985 Transplant media a
8	110	85.9	34	21	AA18732 Amino acid sequenc
9	110	85.9	34	22	AA18732 Amino acid sequenc

10	110	85.9	34	24	AAE34434 Frog dermasptin p
11	105	82.0	34	21	AA18733 Amino acid sequenc
12	105	82.0	34	23	AAU90986 Transplant media a
13	99.5	77.7	32	19	AAW6438 Cationic peptide d
14	99.5	77.7	32	21	AAU91737 Cationic peptide d
15	99.5	77.7	32	24	AAU59614 Cationic cancer -t
16	59	46.1	30	21	AAU87377 Cationic anticirc
17	54.5	42.6	417	16	AAE66223 Cystathionine gamm
18	54	42.2	29	21	AAU87376 Cationic antimicro
19	54	42.2	29	21	AAU87378 Cationic antimicro
20	51.5	40.2	31	21	AA18728 Amino acid sequenc
21	50	39.1	30	21	AA18731 Human liver peptid
22	49	38.3	287	22	ABG49743 Peptide #2384 enco
23	49	38.3	287	22	ABE29733 Peptide #2384 enco
24	49	38.3	287	22	AAU55715 Human brain expres
25	49	38.3	287	22	AAU68093 Human bone marrow
26	49	38.3	287	22	AAU15917 Peptide #2351 enco
27	49	38.3	287	22	AAU03653 Peptide #2335 enco
28	48.5	37.9	30	21	AA18734 Amino acid sequenc
29	48.5	37.9	30	23	AAU90987 Transplant media a
30	48.5	37.9	36	21	AA18727 Amino acid sequenc
31	48	37.5	171	22	AAU16272 Human novel secret
32	48	37.5	171	24	AAU55341 Human novel polype
33	48	37.5	336	24	ABJ37876 GPR7 ligand relate
34	48	37.5	723	21	AAU75477 Neisseria meningit
35	48	37.5	1274	22	AAU79202 Corynebacterium gl
36	48	37.5	1295	22	AAU92726 C glutamicum prote
37	47.5	37.1	590	23	AAE17085 Arabidopsis thalia
38	47.5	37.1	642	23	AAE17088 Arabidopsis thalia
39	47	36.7	29	23	AAU90994 Transplant media a
40	47	36.7	269	22	AAU76593 Corynebacterium gl
41	47	36.7	288	22	AAU90532 C glutamicum prote
42	47	36.7	391	24	ABF77997 N. gonorrhoeae ami
43	47	36.7	403	7	AAU60274 Sequence of creati
44	47	36.7	403	9	AAU90680 Creatine amidohydr
45	46	35.9	28	23	ABB83807 Large puling toad

ALIGNMENTS

RESULT 1  
AA18725

ID AA18725 standard; Protein; 27 AA.

XX AA18725;

AC AA18725;

XX 22-JAN-2001 (first entry)

DT Amino acid sequence of mature protein dermasptin b.

DE Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;

XX cationic peptide; pathogen resistance.

XX Phyllomedusa bicolor.

OS Phyllomedusa bicolor.

XX WO20005337-A1.

PN 21-SEP-2000.

PD 16-MAR-2000; 2000WO-CA00288.

PF 17-MAR-1999; 99US-0125072.

XX (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.

XX Misra S, Kay WD;

XX WPI; 2000-647077/62.

XX Transgenic plants resistant to broad spectrum of pathogens useful for

PT producing biologically active cationic peptides, comprises nucleic acid

PT molecule encoding temporin and/or dermasptin peptides



DE A mature dermaseptin protein with a N-terminal extension.  
 XX Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;  
 KW cationic peptide; pathogen resistance.  
 XX  
 OS Synthetic.  
 XX Phyllomedusa bicolor.  
 XX WO200055337-A1.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 16-MAR-2000; 2000WO-CA00288.  
 XX  
 XX 17-MAR-1999; 99US-0125072.  
 XX  
 XX (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.  
 XX  
 XX Misra S, Kay WD;  
 XX WPI; 2000-647077/62.  
 XX N-PSDB; AAA75751.  
 XX  
 XX Transgenic plants resistant to broad spectrum of pathogens useful for  
 PT producing biologically active cationic peptides, comprises nucleic acid  
 PT molecule encoding temporin and/or dermaseptin peptides  
 XX  
 XX Example; Page 51; 58pp; English.  
 XX  
 XX The present sequence represents a mature dermaseptin polypeptide  
 CC which has a N-terminal extension. Dermaseptin has antibacterial  
 CC activity, and inhibits fungal growth. Cationic peptides derived from  
 CC temporins and dermaseptins are used to produce transgenic plants. The  
 CC transgenic plants are useful for producing biologically active cationic  
 CC peptides such as temporins and dermaseptins in large quantities. The  
 CC peptide confers broad spectrum pathogen resistance including enhanced  
 CC resistance to both fungal and bacterial pathogens in the transgenic  
 CC plants. The transgenic plants may be used in conventional agricultural  
 CC applications such as food crops, medical and other applications.  
 XX  
 XX Sequence 32 AA;  
 SQ  
 Query Match 100.0%; Score 128; DB 21; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DVLKKGITVALHAGKAALGAVADTISQ 27  
 DB 6 DVLKKGITVALHAGKAALGAVADTISQ 32  
 RESULT 5  
 AAB18724  
 ID AAB18724 standard; Protein; 78 AA.  
 XX  
 XX AAB18724;  
 XX  
 XX 22-JAN-2001 (first entry)  
 XX  
 XX A dermaseptin precursor polypeptide.  
 DE Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;  
 KW cationic peptide; pathogen resistance.  
 XX  
 XX Phyllomedusa bicolor.  
 XX WO200055337-A1.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 16-MAR-2000; 2000WO-CA00288.  
 XX  
 XX 17-MAR-1999; 99US-0125072.

XX (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.  
 XX Misra S, Kay WD;  
 XX WPI; 2000-647077/62.  
 XX N-PSDB; AAA75749.  
 XX  
 XX Transgenic plants resistant to broad spectrum of pathogens useful for  
 PT producing biologically active cationic peptides, comprises nucleic acid  
 PT molecule encoding temporin and/or dermaseptin peptides  
 XX  
 XX Disclosure; Page 47; 58pp; English.  
 XX  
 XX The present sequence represents a dermaseptin precursor polypeptide.  
 CC The precursor is processed to produce two mature forms, dermaseptin b  
 CC (AAB18725) and dermaseptin B (AAB18726). Dermaseptin has antibacterial  
 CC activity, and inhibits fungal growth. Cationic peptides derived from  
 CC temporins and dermaseptins are used to produce transgenic plants. The  
 CC transgenic plants are useful for producing biologically active cationic  
 CC peptides such as temporins and dermaseptins in large quantities. The  
 CC peptide confers broad spectrum pathogen resistance including enhanced  
 CC resistance to both fungal and bacterial pathogens in the transgenic  
 CC plants. The transgenic plants may be used in conventional agricultural  
 CC applications such as food crops, medical and other applications.  
 XX  
 XX Sequence 78 AA;  
 SQ  
 Query Match 100.0%; Score 128; DB 21; Length 78;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-12;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DVLKKGITVALHAGKAALGAVADTISQ 27  
 DB 49 DVLKKGITVALHAGKAALGAVADTISQ 75  
 RESULT 6  
 AAY87380  
 ID AAY87380 standard; peptide; 33 AA.  
 XX  
 XX AAY87380;  
 XX  
 XX 03-JUL-2000 (first entry)  
 XX  
 XX Cationic antimicrobial peptide DER (frog dermaseptin), SEQ ID NO:23.  
 DE Antimicrobial; cationic; antibacterial; antiproliferative;  
 KW endotoxaemia; sepsis; wound repair; tissue regeneration;  
 KW transgenic animal; pathogen resistance.  
 XX  
 XX Anura.  
 OS  
 XX WO200012528-A1.  
 XX  
 XX 09-MAR-2000.  
 XX  
 XX 27-AUG-1999; 99WO-US19646.  
 XX  
 XX 28-AUG-1998; 98US-0143124.  
 XX  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 XX Hancock RW, Gough MA, Patrzykat A, Woods D, Jia X;  
 PI WPI; 2000-270790/23.  
 XX  
 XX Novel anti-endotoxic, antimicrobial cationic peptides useful for  
 PT inhibiting endotoxaemia/sepsis-associated disorder or cell  
 PT proliferation, accelerating wound healing, and treating respiratory  
 PT associated disorder  
 XX  
 XX Claim 17; Page 93; 116pp; English.

XX CC The invention relates to a novel class of cationic antimicrobial peptides (AAV87358-Y87381 and AAV87383-Y87391). It also encompasses nucleotides encoding the peptides and a transgenic animal comprising a nucleotide sequence encoding an anti-microbial peptide. The cationic antimicrobial peptides of the invention are useful for inhibiting the growth of Gram positive or Gram negative bacteria, in combination with an antibiotic or lysozyme. The peptides are also useful for inhibiting the growth of a eukaryotic cell e.g., a neoplastic cell, and sequences AAV87358-Y87369 may be used for inhibiting cell proliferation-associated disorders such as cancer. Peptides AAV87360-Y87369 are useful for inhibiting endotoxaemia or a sepsis-associated disorder such as septic shock. The peptides of the invention may also be used for accelerating wound repair in a patient when coadministered with a healing agent such as TGF-beta (transforming growth factor-beta). The peptides are used for treating a respiratory or pulmonary-associated infection, or a disorder such as cystic fibrosis. The peptides are used for revitalising scar tissue, for wound repair. The peptides are used for promoting tissue growth and for promoting tissue growth in skin grafts. Nucleic acids encoding peptides AAV87372-Y87378 and AAV87383-Y87391 may be used in the generation of transgenic animals, with nucleotide encoding sequences AAV87372 and AAV87374-Y87378 being particularly useful for the generation of transgenic fish with enhanced resistance to pathogenic organisms. Sequences AAV87358-Y87381 and AAV87383-Y87391 represent cationic antimicrobial peptides claimed for use in various embodiments of the invention.

XX SQ Sequence 33 AA;

Query Match 85.9%; Score 110; DB 21; Length 33;  
 Best Local Similarity 84.6%; Pred. No. 8e-10; Indels 0; Gaps 0;  
 Matches 22; Conservative 3; Mismatches 1;

Qy 2 VLKKGITVALHAGKAALGAAVADTISQ 27  
 Db 6 MLKKLGTVLHAGKAALGAAADTISQ 31

~ RESULT 7  
 AAU90985  
 ID AAU90985 standard; Peptide; 33 AA.

XX AC AAU90985;  
 XX DT 05-JUN-2002 (first entry)  
 XX DE Transplant media associated antimicrobial peptide #21.  
 XX KW Transplant; antimicrobial peptide; pore forming agent;  
 XX KW cell surface receptor binding compound; kidney transplant;  
 XX KW cardioplegia; organ transplant; transplant rejection.  
 XX OS Phyllomedusa sauvagii.

XX WO200209738-A1.  
 XX PD 07-FEB-2002.  
 XX PF 27-JUL-2001; 2001WO-US23785.  
 XX PR 28-JUL-2000; 2000US-221632P.  
 XX PR 17-NOV-2000; 2000US-249602P.  
 XX PR 15-MAY-2001; 2001US-290932P.

XX PA (MURP/) MURPHY C J.

XX PI Murphy CJ, Reid TW, Mcanulty JP;

XX WI; 2002-268995/31.

XX Media comprising antimicrobial polypeptides or pore forming agents  
 PT and/or cell surface receptor binding compounds useful for the storage  
 PT and preservation of organs prior to transplant -

XX PS Disclosure; Page 26; 78pp; English.  
 XX CC The invention describes new transplant compositions comprising antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds. The media is capable of extending the preservation period past 72 hours and can provide organs with increased functionality upon transplant. Animals receiving kidneys stored in the media of the present invention for either three or four days had serum creatinine levels of less than half of those observed in control animals receiving kidneys stored in UW solution (defined in the specification) alone. Lower serum creatinine levels are indicative of healthier kidneys and a more preferable prognosis for the transplant patient. The media of the invention are useful for decreasing the incidence and/or severity of delayed graft function in patients receiving transplanted kidneys stored and/or treated in the media. The media may also be used in procedures such as cardioplegia. It is contemplated that transplant of healthier organs leads to a decrease in chronic rejection. This sequence represents an antimicrobial peptide studied in the development of the transplant media.

SQ Sequence 33 AA;

Query Match 85.9%; Score 110; DB 23; Length 33;  
 Best Local Similarity 84.6%; Pred. No. 8e-10; Indels 0; Gaps 0;  
 Matches 22; Conservative 3; Mismatches 1;

Qy 2 VLKKGITVALHAGKAALGAAVADTISQ 27  
 Db 6 MLKKLGTVLHAGKAALGAAADTISQ 31

RESULT 8  
 AAB18732  
 ID AAB18732 standard; Protein; 34 AA.

XX AC AAB18732;

XX DT 22-JAN-2001 (first entry)

XX DE Amino acid sequence of a mature processed form of dermaseptin.

XX KW Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;  
 XX KW cationic peptide; pathogen resistance.

XX OS Phyllomedusa sauvagii.

XX WO200005337-A1.

XX PD 21-SEP-2000.

XX PF 16-MAR-2000; 2000WO-CA00288.

XX PR 17-MAR-1999; 99US-0125072.

XX PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.

XX PI Miera S, Kay WD;

XX WI; 2000-647077/62.

XX Transgenic plants resistant to broad spectrum of pathogens useful for  
 PT producing biologically active cationic peptides, comprises nucleic acid  
 PT molecule encoding temporin and/or dermaseptin peptides -

XX Claim 3; Page 49; 58pp; English.

XX AAB18725-36 represent mature processed forms of dermaseptin. Dermaseptin  
 CC has antibacterial activity, and inhibits fungal growth. Cationic  
 CC peptides derived from temporins and dermaseptins are used to produce  
 CC transgenic plants. The transgenic plants are useful for producing  
 CC biologically active cationic peptides such as temporins and dermaseptins  
 CC in large quantities. The peptide confers broad spectrum pathogen

CC resistance including enhanced resistance to both fungal and bacterial  
 CC pathogens in the transgenic plants. The transgenic plants may be used  
 CC in conventional agricultural applications such as food crops, medical  
 CC and other applications.

XX SQ Sequence 34 AA;  
 Query Match 85.9%; Score 110; DB 21; Length 34;  
 Best Local Similarity 84.6%; Pred. No. 8.3e-10;  
 Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 VLKKGITVALHAGKAALGAVADTISQ 27  
 :|||:|||||  
 Db 6 MLKKGITVALHAGKAALGAAADTISQ 31

RESULT 9  
 AAB91864  
 ID AAB91864 standard; Peptide; 34 AA.

XX AC AAB91864;  
 DT 22-JUN-2001 (first entry)

XX DE Antimicrobial peptide SEQ ID NO:1040.

XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimide; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.  
 OS Synthetic.

XX PN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US13576.

XX PR 17-MAY-1999; 99US-0134406.

XX PR 10-SEP-1999; 99US-0153406.

XX PR 15-OCT-1999; 99US-0159783.

XX PA (CONJ-) CONJUCHEM INC.

XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibadeau K;

XX DR WPI; 2001-112059/12.

XX PT Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity

XX PS Disclosure; Page 536; 733pp; English.

XX CC The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimide and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.

XX

SQ Sequence 34 AA;

Query Match 85.9%; Score 110; DB 22; Length 34;  
 Best Local Similarity 84.6%; Pred. No. 8.3e-10;  
 Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 VLKKGITVALHAGKAALGAVADTISQ 27  
 :|||:|||||  
 Db 6 MLKKGITVALHAGKAALGAAADTISQ 31

RESULT 10  
 AAE34434  
 ID AAE34434 standard; peptide; 34 AA.

XX AC AAE34434;

XX DT 14-MAY-2003 (first entry)

XX DE Frog dermaseptin peptide.

XX KW Antimicrobial; purple blotch; gene therapy; antibacterial; fungicide;  
 KW frog; dermaseptin.

XX OS Rana sp.

XX PN WO200295076-A2.

XX PD 28-NOV-2002.

XX PF 17-MAY-2002; 2002WO-JP04800.

XX PR 23-MAY-2001; 2001JP-0154321.

XX PR 26-DEC-2001; 2001JP-0394821.

XX PA (TOYU) TOYOTA CHUO KENYUSHO KK.

XX PI Muramoto N, Imaeda T, Hirai M, Shimamura T;

XX DR WPI; 2003-156762/15.

XX PT New polypeptide comprising at least one protease-resistant or  
 PT protease-sensitive sequence, bound to the C-terminal side of the target  
 PT polypeptide, useful as antimicrobial agent against Ceratocystis  
 PT fimbriata, or Escherichia coli -

XX PS Example 14; Fig 5; 50pp; English.

XX CC The invention relates to a polypeptide comprising at least one protease-  
 CC resistant or protease-sensitive sequence, bound to the C-terminal side  
 CC of the target polypeptide. The polypeptides are useful as antimicrobial  
 CC agents against Ceratocystis fimbriata, which causes purple blotch in  
 CC sweet potatoes, or Escherichia coli. They are also used in gene therapy.  
 CC The present sequence is frog dermaseptin peptide used in the  
 CC exemplification of the invention.

XX SQ Sequence 34 AA;

Query Match 85.9%; Score 110; DB 24; Length 34;  
 Best Local Similarity 84.6%; Pred. No. 8.3e-10;  
 Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 VLKKGITVALHAGKAALGAVADTISQ 27  
 :|||:|||||  
 Db 6 MLKKGITVALHAGKAALGAAADTISQ 31

RESULT 11

AAB18733  
 ID AAB18733 standard; Protein; 34 AA.

XX AC AAB18733;

XX

DT 22-JAN-2001 (first entry)  
 DE Amino acid sequence of a mature processed form of dermaseptin.  
 XX Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;  
 KW cationic peptide; pathogen resistance.  
 XX Phyllomedusa sauvagei.  
 OS WO200055337-A1.  
 PN 21-SEP-2000.  
 XX 16-MAR-2000; 2000WO-CA00288.  
 PD 17-MAR-1999; 99US-0125072.  
 PP (UVVI-) UNIV VICTORIA INNOVATION & DEV CORP.  
 PR Misra S, Kay WD;  
 XX WPI, 2000-647077/62.  
 XX Transgenic plants resistant to broad spectrum of pathogens useful for  
 PT producing biologically active cationic peptides, comprises nucleic acid  
 PT molecule encoding temporin and/or dermaseptin peptides -  
 XX Claim 3; Page 49; 58pp; English.  
 XX AAB18725-36 represent mature processed forms of dermaseptin. Dermaseptin  
 CC has antibacterial activity, and inhibits fungal growth. Cationic  
 CC peptides derived from temporins and dermaseptins are used to produce  
 CC transgenic plants. The transgenic plants are useful for producing  
 CC biologically active cationic peptides such as temporins and dermaseptins  
 CC in large quantities. The peptide confers broad spectrum pathogen  
 CC resistance including enhanced resistance to both fungal and bacterial  
 CC pathogens in the transgenic plants. The transgenic plants may be used  
 CC in conventional agricultural applications such as food crops, medical  
 CC and other applications.  
 XX SQ Sequence 34 AA;  
 Query Match 82.0%; Score 105; DB 21; Length 34;  
 Best Local Similarity 80.8%; Pred. No. 4.9e-09;  
 Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 VLKKGITVALHAGKAAALGAVADTISQ 27  
 DB 6 MLKKLGITMALHAGKAAALGAAANTISQ 31  
 RESULT 12  
 ID AAU90986  
 AC AAU90986 standard; Peptide; 34 AA.  
 XX AAU90986;  
 DT 05-JUN-2002 (first entry)  
 XX Transplant media associated antimicrobial peptide #22.  
 DE Transplant; antimicrobial peptide; pore forming agent;  
 KW cell surface receptor binding compound; kidney transplant;  
 KW cardioplegia; organ transplant; transplant rejection.  
 XX Phyllomedusa sauvagei.  
 OS WO200209738-A1.  
 PN 07-FEB-2002.  
 XX 27-JUL-2001; 2001WO-US23785.  
 PP (MICK-) MICROLOGIX BIOTECH INC.  
 XX

PR 28-JUL-2000; 2000US-221632P.  
 PR 17-NOV-2000; 2000US-249602P.  
 XX 15-MAY-2001; 2001US-290932P.  
 PA (MURP/) MURPHY C J.  
 XX Murphy CJ, Reid TW, Mcanulty JF;  
 PI WPI; 2002-268995/31.  
 XX Media comprising antimicrobial polypeptides or pore forming agents  
 XX and/or cell surface receptor binding compounds useful for the storage  
 XX and preservation of organs prior to transplant -  
 PS Disclosure; Page 26; 78pp; English.  
 XX The invention describes new transplant compositions comprising  
 CC antimicrobial polypeptides or pore forming agents and/or cell surface  
 CC receptor binding compounds. The media is capable of extending the  
 CC preservation period past 72 hours and can provide organs with increased  
 CC functionality upon transplant. Animals receiving kidneys stored in the  
 CC media of the present invention for either three or four days had serum  
 CC creatinine levels of less than half of those observed in control animals  
 CC receiving kidneys stored in UW solution (defined in the specification)  
 CC alone. Lower serum creatinine levels are indicative of healthier kidneys  
 CC and a more preferable prognosis for the transplant patient. The media of  
 CC the invention are useful for decreasing the incidence and/or severity of  
 CC delayed graft function in patients receiving transplanted kidneys stored  
 CC and/or treated in the media. The media may also be used in procedures  
 CC such as cardioplegia. It is contemplated that transplant of healthier  
 CC organs leads to a decrease in chronic rejection. This sequence represents  
 CC an antimicrobial peptide studied in the development of the transplant  
 CC media.  
 XX SQ Sequence 34 AA;  
 Query Match 82.0%; Score 105; DB 23; Length 34;  
 Best Local Similarity 80.8%; Pred. No. 4.9e-09;  
 Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 VLKKGITVALHAGKAAALGAVADTISQ 27  
 DB 6 MLKKLGITMALHAGKAAALGAAANTISQ 31  
 RESULT 13  
 ID AAW66438  
 AC AAW66438 standard; peptide; 32 AA.  
 XX AAW66438;  
 DT 12-JAN-1999 (first entry)  
 XX Cationic peptide dermaseptin.  
 DE Indolicidin analogue; resistance; cationic peptide; antibiotic;  
 XX bacterial infection; tolerance; antibacterial; microorganism;  
 KW bacteria; fungus; parasite; virus.  
 XX Phyllomedusa sauvagei.  
 OS WO9840401-A2.  
 PN 17-SEP-1998.  
 XX 10-MAR-1998; 98WO-CA00190.  
 XX 25-FEB-1998; 98US-0030619.  
 PR 10-MAR-1997; 97US-0040649.  
 PR 20-AUG-1997; 97US-0915314.  
 PR 26-SEP-1997; 97US-0060099.  
 XX (MICK-) MICROLOGIX BIOTECH INC.  
 PA



XX PI Fraser JR, McNicol PJ, West MHP;  
 XX DR WPI; 1998-520800/44.  
 XX PT New indolicidin peptide analogues - useful for, e.g. enhancing  
 XX PT activity of antibiotic or overcoming tolerance, acquired resistance  
 XX PT or inherent resistance of microorganisms  
 XX PS Disclosure; Page 10; 105pp; English.  
 XX CC AAM66393 to AAM66469 represent native cationic peptides from the  
 XX CC present invention. The present invention describes compositions and  
 XX CC methods for treating infection, especially bacterial infections. The  
 XX CC compositions and methods use cationic peptides in combination with an  
 XX CC antibiotic agent which are then administered to a patient to enhance the  
 XX CC activity of the antibiotic agent, to overcome: (a) tolerance; (b)  
 XX CC acquired resistance; and (c) inherent resistance. The combinations of  
 XX CC antibiotics and cationic peptides can provide synergistic activity  
 XX CC against a microorganism that is tolerant, inherently resistant, or has  
 XX CC acquired resistance to an antibiotic agent. They can be used for killing  
 XX CC e.g. bacteria, fungi, parasites and viruses.  
 XX SQ Sequence 32 AA;

Query Match 77.7%; Score 99.5; DB 19; Length 32;  
 Best Local Similarity 84.6%; Pred. No. 3.2e-08;  
 Matches 22; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 2 VLKKGTVLHAGKAAALGAVADTISQ 27  
 DB 6 MLKKGTMLHAGKAAALGA-ADTISQ 30

RESULT 14  
 AAY91737  
 ID AAY91737 standard; Peptide; 32 AA.

AC AAY91737;

DT 06-JUN-2000 (first entry)

DE Cationic peptide Dermaseptin amino acid sequence.

XX CC Cationic peptide; tumour; pharmaceutical composition; cancer; treatment;  
 XX KW leukaemia; polyoxalkylene-modified; APO; lymphoma; multiple myeloma;  
 XX KW breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;  
 XX KW multidrug resistance.

XX OS Unidentified.

XX PN WO9965506-A2.

XX PD 23-DEC-1999.

XX PF 14-JUN-1999; 99WO-CA00552.

XX PR 12-JUN-1998; 98US-0096541.

XX PA (MICR-) MICROLOGIX BIOTECH INC.

XX PI Friedland HD, Krieger TV, Taylor R, Erfle D, Fraser JR, West MHP;  
 XX DR WPI; 2000-223549/19.

XX PT Novel pharmaceutical composition containing optionally activated  
 XX PT polyoxalkylene-modified cationic peptides, useful for treating tumours  
 XX PT

XX PS Disclosure; Page 11; 94pp; English.

XX CC This sequence represents a cationic peptide amino acid sequence, which  
 XX CC can be used in the pharmaceutical composition of the invention. The

CC invention relates to a pharmaceutical composition containing at least one  
 CC activated polyoxalkylene (APO)-modified cationic peptide. The  
 CC modification of peptides with APO increases their activity against tumour  
 CC cells, including those with a multidrug resistant phenotype. The  
 CC pharmaceutical composition can be used to treat tumours, specifically  
 CC lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary,  
 XX cervix, uterus, skin, prostate, liver and colon.

XX SQ Sequence 32 AA;

Query Match 77.7%; Score 99.5; DB 21; Length 32;  
 Best Local Similarity 84.6%; Pred. No. 3.2e-08;  
 Matches 22; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 2 VLKKGTVLHAGKAAALGAVADTISQ 27  
 DB 6 MLKKGTMLHAGKAAALGA-ADTISQ 30

RESULT 15  
 ABUS9614  
 ID ABUS9614 standard; Peptide; 32 AA.

XX AC ABUS9614;

XX DT 22-APR-2003 (first entry)

DE Cationic cancer -targeting peptide #46.

XX KW Targeting ligand; bioactive agent; polymer matrix; cancer; cytostatic;  
 XX KW cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor;  
 XX KW fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;  
 XX KW tumour; cationic cancer-targeting peptide.

XX OS Synthetic.

XX PN US2002041898-A1.

XX PD 11-APR-2002.

XX PF 25-JUL-2001; 2001US-0912609.

XX PR 05-JAN-2000; 2000US-0478124.

XX PR 31-OCT-2000; 2000US-0703474.

XX PA (UNGE/) UNGER E C.

XX PA (MATS/) MATSUNAGA T O.

XX PA (RAMA/) RAMASWAMI V.

XX PA (ROMA/) ROMANOWSKI M J.

XX PI Unger EC, Mateunaga TO, Ramaswami V, Romanowski MJ;

XX DR WPI; 2003-208921/20.

XX PT Targeted delivery system comprising a bioactive agent homogeneously  
 XX PT dispersed in a targeted matrix is especially useful in cancer therapy  
 XX PT

XX PS Disclosure; Page14; 46pp; English.

XX CC The invention relates to a composition comprising a bioactive agent  
 XX CC homogeneously dispersed in a targeted matrix (polymer and targeting  
 XX CC ligand). Also included are a targeted matrix for use as a delivery  
 XX CC vehicle comprising a polymer associated with a targeting ligand,  
 XX CC enhancing the bioavailability of an agent comprising administration of the  
 XX CC of the composition and treating cancer comprising administration of the  
 XX CC novel composition. The method is useful for targeted delivery of a drug,  
 XX CC especially in cancer therapy. The targeting ligand may be a peptide.  
 XX CC Examples of targeting peptides are disclosed including cathepsin-D  
 XX CC substrate peptides, peptides targeting receptors in the brain and  
 XX CC kidney, peptides recognising fibronectin- and vitronectin-binding  
 XX CC integrins, peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g.,  
 XX CC antibodies, peptides targeting the angiogenic endothelium of solid

CC tumours, tissue specific peptides (e.g. of lung, skin, pancreas,  
 CC intestine, uterus, adrenal gland and retina), and cationic cancer-  
 CC targeting peptides. The present sequence is a peptide targeting  
 CC ligand disclosed in the invention.

XX  
 SQ Sequence 32 AA;

Query Match 77.7%; Score 99.5; DB 24; Length 32;  
 Best Local Similarity 84.6%; Pred. No. 3.2e-08;  
 Matches 22; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 2 VLKIGTVALHAGKALGAVDTISQ 27  
 Db 6 MLKLGTVLHAGKALGAVDTISQ 30

Search completed: December 10, 2003, 20:27:42  
 Job time : 42 secs